RAW SEQUENCE LISTING ERROR REPORT
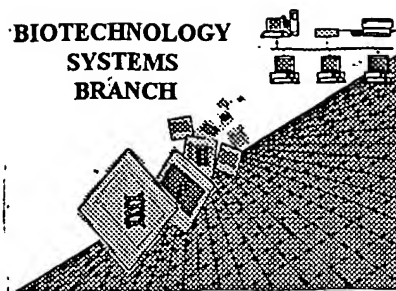
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/009,330*

Source: *PCT/10*

Date Processed by STIC: *1/14/2002*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
        Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *10/009,330*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFT

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) *10* missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING   DATE: 01/14/2002
PATENT APPLICATION: US/10/009,330   TIME: 13:43:57

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF3\01142002\J009330.raw**

Does Not Comply
Corrected Diskette Needed

```
        3 <110> APPLICANT: Takeda Chemical Industries, Ltd.
W--)    4 <120> TITLE OF INVENTION: Screening Method Using CD100
W--)    5 <130> FILE REFERENCE: 2611WOOP
C--)    6 <140> CURRENT APPLICATION NUMBER: US/10/009,330
C--)    6 <141> CURRENT FILING DATE: 2001-12-03
        6 <150> PRIOR APPLICATION NUMBER: JP 11-157111
        7 <151> PRIOR FILING DATE: 1999-06-03
W--)    8 <160> NUMBER OF SEQ ID: 10
```

·ERRORED SEQUENCES

```
      413 <210> SEQ ID NO: 6        1337 shown
      414 <211> LENGTH: (1357)
      415 <212> TYPE: DNA
      416 <213> ORGANISM: Mouse
W/E-) 417 <400> SEQUENCE: 6
      418 tggaagactg tgaagcagag gcgcccaggg ctatggctga cgctatcacg tatgcagacc    60
      419 tgcgctttgt gaaagtgccc ctgaagaaca gcgcatctaa ccatctagga caggactgtg   120
      420 aggcctatga agatggggaa ctcacctacg agaatgtgca agtgtctcca gtcccaggag   180
      421 ggccaccagg cttggcttcc cctgcactag cggacaaagc aggggtcggg tcagagcaac   240
      422 caactgcgac ctggagctct gtgaactcgt ctgctctcag gcagattccc cgctgtccta   300
      423 cagtctgctt gcaatacttc ttgcttggcc ttctcgtgtc ctgtctgatg ttaggggtgg   360
      424 ctgtcatctg cctgggagtt cgctatctgc aggtgtctcg gcagttccag gaggggacca   420
      425 ggatttggga agccaccaat agcagcctgc agcagcagct cagggagaag ataagtcagc   480
      426 tggggcagaa ggaggtggag cttcagaagg ctcggaaaga gctgatctcg agccaggaca   540
      427 cattacagga gaagcagagg actcacgagg acgctgagca gcaactacaa gcctgccagg   600
      428 ctgagagagc gaagaccaag gagaacctga aaactgagga ggagcggagg agggacctgg   660
      429 accagaggtt gacaagcacg cgggagacac tgaggcgctt cttctctgat tcatcagaca   720
      430 cctgctgtcc atgcggatgg attccatatc aggaaaggtg cttttacatc tcacataccc   780
      431 tcggaagtct ggaggagagc caaaaatact gcacatctct gtcctccaaa ctggcagcat   840
      432 tcgatgaacc ttctaagtat tactatgaag tttctctgcc cagcggctta gaggagttgc   900
      433 tagatcgttc gaagtcatat tggatacaga tgagcaagaa gtggaggcag gactctgact   960
      434 ctcaaagccg acattgtgtc aggataaaaa catattacca gaagtgggaa agaacaattt  1020
      435 ccaagtgtgc agagcttcac ccctgcattt gtgagtcgga ggctttcagg tttcctgatg  1080
      436 ggatcaatct gaactgaaac ggacacttga acaagacctt gtgacctaca tccttaacct  1140
      437 acggcctgcc aattttaag actgctattc ctccagcact ccctcactct cgggcatgcc  1200
      438 cagctaaggg atgacctgct gcttgcttga aagctgctcc agaaactgga cttctcttgg  1260
E--)  439 gaagagtaaa gaagcctcca gaaaagactt gaccttcctt aagaacttcc caaactagag  (1340) 1320
E--)  440 atgggtcagg ggagggc                                                 (1357) 1337
      531 <210> SEQ ID NO: 10
      532 <211> LENGTH: 53
      533 <212> TYPE: DNA
      534 <213> ORGANISM: (Artificial Sequence)  —)   see item 11 on Error Summary Sheet
W--)  535 <220> FEATURE:
      536 <223> OTHER INFORMATION:
W/E-) 537 <400> SEQUENCE: 10
```

see next page

RAW SEQUENCE LISTING   DATE: 01/14/2002
PATENT APPLICATION: US/10/009,330   TIME: 13:43:57

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\01142002\J009330.raw

538 gacggatcct acttactttg ctttgcttgc ttgagataca ccgtcttctc tga   53

E--> 543 (1)

delete

VERIFICATION SUMMARY   DATE: 01/14/2002
PATENT APPLICATION: US/10/009,330   TIME: 13:43:58

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF3\01142002\J009330.raw**

```
L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:9 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <400> field identifier
L:126 M:283 W: Missing Blank Line separator, <400> field identifier
L:178 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:283 W: Missing Blank Line separator, <400> field identifier
L:366 M:283 W: Missing Blank Line separator, <400> field identifier
L:417 M:283 W: Missing Blank Line separator, <400> field identifier
L:439 M:254 E: No. of Bases conflict, LENGTH:Input:1340 Counted:1320 SEQ:6
M:254 Repeated in SeqNo=6
L:440 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1357 Found:1337 SEQ:6
L:445 M:283 W: Missing Blank Line separator, <400> field identifier
L:496 M:283 W: Missing Blank Line separator, <400> field identifier
L:527 M:283 W: Missing Blank Line separator, <220> field identifier
L:529 M:283 W: Missing Blank Line separator, <400> field identifier
L:535 M:283 W: Missing Blank Line separator, <220> field identifier
L:537 M:283 W: Missing Blank Line separator, <400> field identifier
L:543 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:53 SEQ:10
```